Co. letters

1636

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/430,590D

DATE: 04/17/2001
TIME: 14:36:46

Input Set : A:\PTO.txt
Output Set: N:\CRF3\04172001\I430590D.raw

Does Not Comply
Corrected Diskette Needed
See p. 6

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 3 <110> APPLICANT: Poulter, et al.
 5 <120> TITLE OF INVENTION: UNUSUAL RETROTRANSPOSON FROM THE YEAST CANDIDA ALBICANS
 7 <130> FILE REFERENCE: 674521-2001.1
 9 <140> CURRENT APPLICATION NUMBER: 09/430,590D
10 <141> CURRENT FILING DATE: 1999-10-29
12 <150> PRIOR APPLICATION NUMBER: 60/106,342
13 <151> PRIOR FILING DATE: 1998-10-30
15 <160> NUMBER OF SEQ ID NOS: 156
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 388
21 <212> TYPE: DNA
22 <213> ORGANISM: Candida albicans
24 <300> PUBLICATION INFORMATION:
25 <308> DATABASE ACCESSION NO: AF043301
26 <309> DATABASE ENTRY DATE: 1998-07-21
27 <313> RELEVANT RESIDUES: (1)..(388)
29 <400> SEQUENCE: 1
30 tgttcgctat agagagattt cctagccgga atgcacgaca atcctgagac ggaagtcgat     60
32 cgtcgatgcc catggtgcgt ggtgaaaaat tttcttagaa aatttgttct ttccttcaac    120
34 tgcttttaag aaagagaggt tcaagtggtt taagtacgac ggtcacaaag attgcggctt    180
36 atgaggcccg aactgagttg aaatacaaaa tcaagatata attatatacc ttacttgtcc    240
38 atattgtttt ataatacatt cttcagatat ttaaatttct gtgtatcaac ctataaaaca    300
40 gagatacatt cagtgcattt agtatactga gtgaactggt acctgtgaca ttcaagataa    360
42 ctgtttcgcg cacgctggca gacgaaca                                      388
45 <210> SEQ ID NO: 2
46 <211> LENGTH: 400
47 <212> TYPE: DNA
48 <213> ORGANISM: Candida albicans
50 <300> PUBLICATION INFORMATION:
51 <308> DATABASE ACCESSION NO: Y08494
52 <309> DATABASE ENTRY DATE: 1997-08-27
53 <313> RELEVANT RESIDUES: (1)..(400)
55 <400> SEQUENCE: 2
56 cgggttaatg tatatttcga cttgcaggac ctatagaaca gctgtagatg taaacactaa     60
58 tatgaagaac tgggaaaaca ataacttcta ttctgactct gattctgtat gaaaactaac    120
60 tgaagaaaag aatataaaaa tataaaatat ataagaagac aaaggagaat ctctgaccct    180
62 tatatagacc gaaaactaga gtgacgatga accatcagac cagtcaataa ccaactaatt    240
64 taataatatc aataactcgt ctaacgaggt gtaaacaaaa taccgaaaat agaaatataa    300
66 ataactcaat gccaagatgg tgcgcaacca ccaaggtaat aaacaaccaa tagaaccaag    360
68 aattgtaaat cagacaacga gcaaggctga ttatacaaca                         400
71 <210> SEQ ID NO: 3
72 <211> LENGTH: 6426
73 <212> TYPE: DNA
74 <213> ORGANISM: Candida albicans
76 <220> FEATURE:
77 <221> NAME/KEY: CDS
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78 <222> LOCATION: (398)..(1372)
79 <223> OTHER INFORMATION: ORF1 coding sequence for gag
82 <220> FEATURE:
83 <221> NAME/KEY: CDS
84 <222> LOCATION: (1373)..(6103)
85 <223> OTHER INFORMATION: ORF2 - coding sequence for pol
88 <400> SEQUENCE: 3
89 tgttggtttg tgcactattt tgtgtcagaa actgatcaat gaaaatgatg gttattatga     60
91 gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt    120
93 ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt    180
95 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacaa ctagacgtgt    240
97 acacgctcaa tctcaggtaa agaaagttta tattccatca gattagaagt cgatagtgat    300
99 aatcatttcg tcccaaatta gcgttgtata aattcagtcc tcagatttgt attattgatt    360
101 gatagtttcg aagtttgaag gtacagaatt tcacaag atg agt tcc gca aag aat     415
102                                          Met Ser Ser Ala Lys Asn
103                                          1               5
105 gat gat aac gaa ggg aag gtc atg gaa agt gtt gat caa gct aat gct      463
106 Asp Asp Asn Glu Gly Lys Val Met Glu Ser Val Asp Gln Ala Asn Ala
107             10                  15                  20
109 att agt aag gtg gat gaa cat atc aag gct aga ttc aat atg ctt ttc      511
110 Ile Ser Lys Val Asp Glu His Ile Lys Ala Arg Phe Asn Met Leu Phe
111         25                  30                  35
113 ata aaa ttt aat gac tta cct aag ttg gcc gtc ggt aat cag aaa agc      559
114 Ile Lys Phe Asn Asp Leu Pro Lys Leu Ala Val Gly Asn Gln Lys Ser
115     40                  45                  50
117 gtg gat aaa tgg aat gaa gaa ttt aaa tat ttc cac gtt gct tac ccc      607
118 Val Asp Lys Trp Asn Glu Glu Phe Lys Tyr Phe His Val Ala Tyr Pro
119 55                  60                  65                  70
121 gat gtt ttg gaa ttt ttg ctt gac tat aat cct aaa gat aaa ttc aag      655
122 Asp Val Leu Glu Phe Leu Leu Asp Tyr Asn Pro Lys Asp Lys Phe Lys
123                 75                  80                  85
125 gtt aaa aag gta gaa ggt att tat ttt act ggt tgg tgt tta caa atg      703
126 Val Lys Lys Val Glu Gly Ile Tyr Phe Thr Gly Trp Cys Leu Gln Met
127             90                  95                  100
129 tgt tta cag tcc att ttt gat agg ttc aga ttg atc atg att tct aag      751
130 Cys Leu Gln Ser Ile Phe Asp Arg Phe Arg Leu Ile Met Ile Ser Lys
131         105                 110                 115
133 cta cca aag cac ttg caa aag gaa gca aac tta atc aaa gct gct tat      799
134 Leu Pro Lys His Leu Gln Lys Glu Ala Asn Leu Ile Lys Ala Ala Tyr
135     120                 125                 130
137 gat gct gtt act aaa tct aaa gat tat acc att act agt aag atc ttg      847
138 Asp Ala Val Thr Lys Ser Lys Asp Tyr Thr Ile Thr Ser Lys Ile Leu
139 135                 140                 145                 150
141 ctg aag ttt gta aac gtt gaa cat gag tta gtg gtt tgc tat aac ctt      895
142 Ser Lys Phe Val Asn Val Glu His Glu Leu Val Val Cys Tyr Asn Leu
143                 155                 160                 165
145 cca tat ttg ctg cag gtg gaa gag aaa ctt gag gaa ata ctc tac aac      943
146 Pro Tyr Leu Ser Gln Val Glu Glu Lys Leu Glu Glu Ile Leu Tyr Asn
147             170                 175                 180
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149 act tca aac gtt gtc gat gag tat gtc cgt agt ctt cca aat ctc ata      991
150 Thr Ser Asn Val Val Asp Glu Tyr Val Arg Ser Leu Pro Asn Leu Ile
151         185                 190                 195
153 ggt caa gtc ttg tac ttc aat cat gtg aag aaa tca gag gct tta agt     1039
154 Gly Gln Val Leu Tyr Phe Asn His Val Lys Lys Ser Glu Ala Leu Ser
155     200                 205                 210
157 ttg ttt ttg aat att cat gcc tca tac tac tca aag tgg att caa gct     1087
158 Leu Phe Leu Asn Ile His Ala Ser Tyr Tyr Ser Lys Trp Ile Gln Ala
159 215                 220                 225                 230
161 gac aat gat aca tca gta ctc cca agt tgc tct acc ata gct gaa gaa     1135
162 Asp Asn Asp Thr Ser Val Leu Pro Ser Cys Ser Thr Ile Ala Glu Glu
163                 235                 240                 245
165 atg tgt gat cat cct gat tat gct aga ttg gtt gac att cca agc aac     1183
166 Met Cys Asp His Pro Asp Tyr Ala Arg Leu Val Asp Ile Pro Ser Asn
167             250                 255                 260
169 aaa tat gaa ctt aat ctt att gtt agt tta cca gca cca gag aaa cca     1231
170 Lys Tyr Glu Leu Asn Leu Ile Val Ser Leu Pro Ala Pro Glu Lys Pro
171         265                 270                 275
173 aaa gga aaa cca gag gag aac tca ctg gaa caa tct caa aag aag aac     1279
174 Lys Gly Lys Pro Glu Glu Asn Ser Ser Glu Gln Ser Gln Lys Lys Asn
175     280                 285                 290
177 ctg aaa tca aga aag aga aat aag aaa cat cca aaa tca gat aac gat     1327
178 Ser Lys Ser Arg Lys Arg Asn Lys Lys His Pro Lys Ser Asp Asn Asp
179 295                 300                 305                 310
181 aaa ggt gaa aaa gaa aaa gaa aaa gaa aaa act tca ctg gaa tga aaa     1375
182 Lys Gly Glu Lys Glu Lys Glu Lys Glu Lys Thr Ser Ser Glu     Lys
183                 315                 320                 325
185 aca ggt gct gct tct att aat tgt gta atg aat ata cat aat tgc agc     1423
186 Thr Gly Ala Ala Ser Ile Asn Cys Val Met Asn Ile His Asn Cys Ser
187                 330                 335                 340
189 aaa acc acg ttt cca gta gaa aat tct cat tct ctt aat gct tct ttg     1471
190 Lys Thr Thr Phe Pro Val Glu Asn Ser His Ser Leu Asn Ala Ser Leu
191             345                 350                 355
193 aac gta atg aat ttt aaa ggt tta agg ttt aac aag tat cta gtg tat     1519
194 Asn Val Met Asn Phe Lys Gly Leu Arg Phe Asn Lys Tyr Leu Val Tyr
195         360                 365                 370
197 gat act ggt gcc aca ata tct gtt gtg aac aat aaa gat ata ttg ctg     1567
198 Asp Thr Gly Ala Thr Ile Ser Val Val Asn Asn Lys Asp Ile Leu Ser
199     375                 380                 385
201 aat gtt aag gac gca aca att gaa gtt tct gtt gct gat ggt gct aca     1615
202 Asn Val Lys Asp Ala Thr Ile Glu Val Ser Val Ala Asp Gly Ala Thr
203 390                 395                 400                 405
205 tta gaa gca gat tgt att ggt gat cta att atc aga gtc ggt att gtc     1663
206 Leu Glu Ala Asp Cys Ile Gly Asp Leu Ile Ile Arg Val Gly Ile Val
207                 410                 415                 420
209 tcg att acg tta gag aat aca ttg tat tta cca gaa agt tcc ttt aat     1711
210 Ser Ile Thr Leu Glu Asn Thr Leu Tyr Leu Pro Glu Ser Ser Phe Asn
211             425                 430                 435
213 ctt gtg agt ttg aaa caa att gaa gaa cga gga ttt aat gtt ctt att     1759
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214 Leu Val Ser Leu Lys Gln Ile Glu Glu Arg Gly Phe Asn Val Leu Ile
215         440                 445                 450
217 act aaa gaa tca gtg att gta ttt aac caa aat gtg gct cct act att     1807
218 Thr Lys Glu Ser Val Ile Val Phe Asn Gln Asn Val Ala Pro Thr Ile
219     455                 460                 465
221 att gct tca agg aag aat gct gct gat ctt tat atg ggt cct caa ttc     1855
222 Ile Ala Ser Arg Lys Asn Ala Ala Asp Leu Tyr Met Gly Pro Gln Phe
223 470                 475                 480                 485
225 agt gaa gaa tct tta gaa tgt gat ttt gat tat gat ggt ttg gca gat     1903
226 Ser Glu Glu Ser Leu Glu Cys Asp Phe Asp Tyr Asp Gly Leu Ala Asp
227                 490                 495                 500
229 atg ttg tcc aat gct aac caa gat gac aaa gat aaa tca agt atg aat     1951
230 Met Leu Ser Asn Ala Asn Gln Asp Asp Lys Asp Lys Ser Ser Met Asn
231             505                 510                 515
233 gaa atg tca gaa tat caa gaa cat gat tat agt tct cga gca tta ata     1999
234 Glu Met Ser Glu Tyr Gln Glu His Asp Tyr Ser Ser Arg Ala Leu Ile
235         520                 525                 530
237 aat tct ttg acg gag gtt gat gtt tta gat gtt gaa att tcc cca tat     2047
238 Asn Ser Leu Thr Glu Val Asp Val Leu Asp Val Glu Ile Ser Pro Tyr
239     535                 540                 545
241 gga gtt gaa caa ttg cta cca act gga gat aag aac gat att tat aat     2095
242 Gly Val Glu Gln Leu Leu Pro Thr Gly Asp Lys Asn Asp Ile Tyr Asn
243 550                 555                 560                 565
245 ttc cat ttg atg tca aat cat atg tcc att gag aaa atc ttg ttg tta     2143
246 Phe His Leu Met Ser Asn His Met Ser Ile Glu Lys Ile Leu Leu Leu
247                 570                 575                 580
249 caa aaa tac cag ggt ctc gta ctt cac act tca aaa gag agt ctt caa     2191
250 Gln Lys Tyr Gln Gly Leu Val Leu His Thr Ser Lys Glu Ser Leu Gln
251             585                 590                 595
253 aag att gct gat tgt aag gta tgt cta tta tcg aat gcc aaa cag aga     2239
254 Lys Ile Ala Asp Cys Lys Val Cys Leu Leu Ser Asn Ala Lys Gln Arg
255         600                 605                 610
257 agt cac aat cat cat tca gaa aga aaa gcc tcg aga aga cat gag aga     2287
258 Ser His Asn His His Ser Glu Arg Lys Ala Ser Arg Arg His Glu Arg
259     615                 620                 625
261 ctt cat tgt gat act ctc ggt cca ttt agg tcc gaa aat aac aag tgg     2335
262 Leu His Cys Asp Thr Leu Gly Pro Phe Arg Ser Glu Asn Asn Lys Trp
263 630                 635                 640                 645
265 tat tta acg tct gtt ata gat gaa cat acg ggt tac att gaa gga att     2383
266 Tyr Leu Thr Ser Val Ile Asp Glu His Thr Gly Tyr Ile Glu Gly Ile
267                 650                 655                 660
269 att act aaa gac aga aag gta aag gat ctc tta att caa cga tta aag     2431
270 Ile Thr Lys Asp Arg Lys Val Lys Asp Leu Leu Ile Gln Arg Leu Lys
271             665                 670                 675
273 atc tgg aat aat cgg ttt aac gat aag gtg gca tac ttc aga agt gat     2479
274 Ile Trp Asn Asn Arg Phe Asn Asp Lys Val Ala Tyr Phe Arg Ser Asp
275         680                 685                 690
277 aat gct cct gag ttc cca caa cct tct gat tta gct gag ttc ggt att     2527
278 Asn Ala Pro Glu Phe Pro Gln Pro Ser Asp Leu Ala Glu Phe Gly Ile
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279     695                 700                 705
281 tgg agg gag act ata gcg gca tat ctg cct gag ctt aat ggt ctc gcc     2575
282 Trp Arg Glu Thr Ile Ala Ala Tyr Ser Pro Glu Leu Asn Gly Leu Ala
283 710                 715                 720                 725
285 gag gtt gtt aat aaa ttg att tta caa cag att tac agg atc gtt gtg     2623
286 Glu Val Val Asn Lys Leu Ile Leu Gln Gln Ile Tyr Arg Ile Val Val
287                 730                 735                 740
289 aca ctt ggt cca caa ata ctc aag ttg att tat tat gtg att caa tat     2671
290 Thr Leu Gly Pro Gln Ile Leu Lys Leu Ile Tyr Tyr Val Ile Gln Tyr
291             745                 750                 755
293 tct att aca atg atc aac cac act cca cgt cgt tca ctc aag gga caa     2719
294 Ser Ile Thr Met Ile Asn His Thr Pro Arg Arg Ser Leu Lys Gly Gln
295         760                 765                 770
297 acc cct tat ggt tgc tat tat caa tta agt gag gga aat ttc tac cgg     2767
298 Thr Pro Tyr Gly Cys Tyr Tyr Gln Leu Ser Glu Gly Asn Phe Tyr Arg
299     775                 780                 785
301 ttt cct ttt gcc atc gat tgt gtc gtt aca ttt agt aat gcc atc gaa     2815
302 Phe Pro Phe Ala Ile Asp Cys Val Val Thr Phe Ser Asn Ala Ile Glu
303 790                 795                 800                 805
305 aag aac cgt tac gga gtt aca tca act aaa gga gct cct tca tcg atc     2863
306 Lys Asn Arg Tyr Gly Val Thr Ser Thr Lys Gly Ala Pro Ser Ser Ile
307                 810                 815                 820
309 atg ggt gct gtg att ggc tac gct agc gat tgt ttt agt tat tac gtg     2911
310 Met Gly Ala Val Ile Gly Tyr Ala Ser Asp Cys Phe Ser Tyr Tyr Val
311             825                 830                 835
313 ttg cta aaa aat atg cgg tgt gat att atc ctt agc cct aat gtc cgt     2959
314 Leu Leu Lys Asn Met Arg Cys Asp Ile Ile Leu Ser Pro Asn Val Arg
315         840                 845                 850
317 ata ttg cga agc tat gag gtt att aac tcc tat ctc aaa aac tta tcc     3007
318 Ile Leu Arg Ser Tyr Glu Val Ile Asn Ser Tyr Leu Lys Asn Leu Ser
319     855                 860                 865
321 act aca cct atg tca cac att gtt cct atg gct gaa ggt atc cag gga     3055
322 Thr Thr Pro Met Ser His Ile Val Pro Met Ala Glu Gly Ile Gln Gly
323 870                 875                 880                 885
325 agg caa ctg ggc gct cag tac gag gta cgc gga aca tat gtg gaa agt     3103
326 Arg Gln Ser Gly Ala Gln Tyr Glu Val Arg Gly Thr Tyr Val Glu Ser
327                 890                 895                 900
329 gaa tat gac aat aca aat gac gtg atg cac atg ccc aaa gag tca tat     3151
330 Glu Tyr Asp Asn Thr Asn Asp Val Met His Met Pro Lys Glu Ser Tyr
331             905                 910                 915
333 tca gtt cag cca gca tcg ttt act tta act acg ggt aac agt tct aac     3199
334 Ser Val Gln Pro Ala Ser Phe Thr Leu Thr Thr Gly Asn Ser Ser Asn
335         920                 925                 930
337 gaa tat gtt ata aat gat gat cca gta cag att acc att gag aat ccc     3247
338 Glu Tyr Val Ile Asn Asp Asp Pro Val Gln Ile Thr Ile Glu Asn Pro
339     935                 940                 945
341 gat gat ttt tct aac cct ctt caa cta act gaa gaa tca cac gat atg     3295
342 Asp Asp Phe Ser Asn Pro Leu Gln Leu Thr Glu Glu Ser His Asp Met
343 950                 955                 960                 965
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L:1187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
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L:1195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
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L:1199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
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L:1217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
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L:9660 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:148
L:9672 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:149
L:9684 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:150
L:9696 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:151
L:9708 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:152
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L:9756 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:156